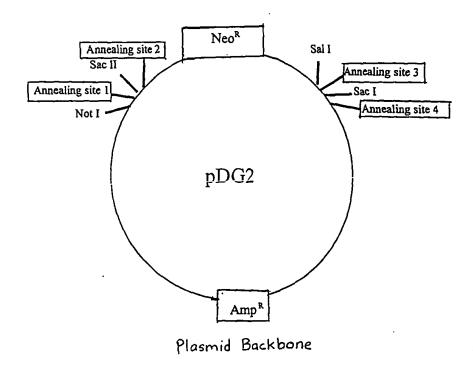


Figure 2A



pDG2:

GTTAACTACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATA TGTATCOGCTCATGAGACAATAACOCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTC CGTGTCGCCCTTATTCCCTTTTTTTGCCGCCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGA TOCTGRAGATCAGTTGGGTGCAGGAGTGGGTTACATCGAACTGGATCTCAACAGGGGTAAGATCCTTGAGAGTTTTTGGCC GAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGA TOGGAGGACOGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATGGTTGGGAACCGGAG CTGAATGAAGOCATAOCAAAOGAOGAGOGTGACAOCAOGATGOCTGTAGCAATGGCAACAAOGTTGGGCAAACTATTAAC GCTCGGCCCTTCCGGCTGGCTGGTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCA CTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGGGTCAGGCAACTATGGATGAACGAAATAG ACAGATOGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTG ATTTACCCCGGTTGATAATCAGAAAAGCCCCAAAAACAGGAAGATTGTATAAGCAAATATTTAAATTGTAAACGTTAATA TTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAAATCCCTTAT AAATCAAAAGAATAGCCCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTC CAACCTCAAAGGGCGAAAAACCGTCTATCAGGGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGGGT OGAGGTGCCGTAAAGCCACTAAATCGGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCGAACGTGGCGA CCCCCCCCCTTAATGCCCCCCTACAGGCCCCTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAA TCCCTTAACGTGAGTTTTCGTTCCACTGAGGGTCAGACCCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTTTT TCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACC ACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTCTTATCCTGTTACCAGTGGCTGCCAGTGGCGATAAG TOCTGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGTTCGTGCAC ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCCTGAGCTATGAGAAAGCGCCACGCTTCCCCG AAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGTCCGGAACAGGAGGCGCGCACGAGGCTTCCAGGGGGAAAC GOCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGGC GAGOCTATGGAAAAACGOCAGCAACGOGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTAATGTG AGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATA ACAATTTCACACAGGAAACAGCTATGAOCATGATTAOGOCAAGCTAOGTAATAOGACTCACTAGGOGGOCGGTTTAAAC AAtqtgctcctctttggcttgcttCCGCCGgccaagccagacaagaaccagTTGACGTCAAGCTTCCCGGGACGCGTGCT AGCGGCGCGCGAATTCCTGCAGGATTCGAGGGCCCCTGCAGGTCAATTCTACCGGGTAGGGGAGGCGCTTTTCCCAAGG CAGTCTGGAGCATGCGCTTTAGCAGCCCCGCTGGCACTTGGCGCTACACAAGTGGCCTCTGGCCTCGCACACATTCCACA TOCACCEGTAGOGCCAACCEGCTCCGTTCTTTGGTGGCCCCTTCGCGCCACCTTCTACTCCCCCTAGTCAGGAAGTTC GGCATTCTCGCACGCTTCAAAAGCGCACGTCTGCCGCGCTGTTCTCCTCTTCCTCATCTCCGGGCCTTTCGACCTGCAGC ACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCCCGGTGTTCCGGCTGTCAGGGCAGGGGCCCCGGTTCTTTTTGTC TTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGTTATTGGGCGAAGTGCCGGGGGAGCATCTCC TGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCGATGCGGCGGCTGCATACGCTTGATCCGGCT ACCTGCCCATTOGACCACCAAGCGAAACATOGCATCGAGCGAGCACGTACTCGGATCGAAGCCGGTCTTGTCGATCAGGA TGATCTGGAGGAAGAGCATCAGGGGCTGGGGCCAGGGGAACTGTTGGCCAGGCTCAAGGGGGCATGGCGGAGGGGATG ATCTOGTOGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGT GGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATG GGCTGACCGCTTCCTCGTGCTTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGT TCTTCTGAGGGGATCGATCCGTGTAAGTCTGCAGAAATTGATGATCTATTAAACAATAAAGATGTCCACTAAAATGG ANGITTITOCTGTCATACTTTGTTAAGAAGGGTGAGAACAGAGTACCTACATTTTGAATGGAAGGATTGGAGCTACGGGG GTGGGGGTGGGGATTAGATAAATGCCTGCTCTTTACTGAAGGCTCTTTACTATTGCTTTATGATAATGTTTCATAG TTGGATATCATAATTTAAACAAGCAAAACCAAATTAAGGGCCAGCTCATTCCTCCCACTCATGATCTATAGATCTATAGA TCTCTCGTGGGATCATTGTTTTTCTCTTGATTCCCACTTTGTGGTTCTAAGTACTGTGGGTTTCCAAATGTGTCAGTTTCA TAGOCTGAAGAAOGAGATCAGCAGOCTCTGTTOCACATACACTTCATTCTCAGTATTGTTTTGOCAAGTTCTAATTCCAT CAGAAGCTGACTCTAGATCTGGATCCGGCCAGCTAGGCCGTCGACCTCGAGTGATCAGGTACCAAggtcctcgctgtg tccgttGAGCTCgacgacacaggacacgcaaaTTAATTAAGGCCGGCCCTACCTCTAGTCAAGGCCTTAAGTGAGTCG TATTACGGACTGGCCGTGGTTTTTACAACGTGGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACA TOCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCCACCGATCGCCTTCCCAACAGTTGCGCAGCCTGAATGGCG

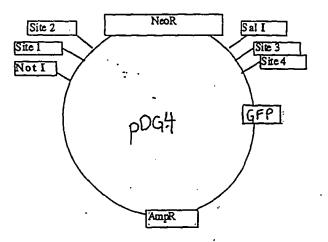


Fig3A

pDG4: PD-C1.
GITTÄÄTAGTAATCÄÄTTAGGGGGATTAGTTCATAGGGCATATATGGAGTTGGGGTTACATAACTTAGGGTAAATGG CONSTRUCTION OF A CONSTRUCTION CHITCHITIGADI GARLIGATOLAGIA TENEGIANATA CENTROCAGIA CALIBRATA CAL GETT: SECTION STEERING TO ANGICTO ACCUPATION OF THE MISSING THE SET THE SECTION AND ANALYMOUS AND ANGICT TO ANGICT AND ANGICT AND ANGICT THE ACCUPATION OF T CTGRETHOCOGGEGOCHOCHTCHCUTCHCOCHOCHCATGAIGCCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCMAGTOCGCACACTICTTCACACACTICTTCACACACTICTTCACACACTICTTCACACACTICTACACTICTTCACACTICTTCACACTICTAC TTGGGTGCACGAGTGCGTTACATCGAACTGGATCTCAACAGGGGTAAGATGTTGAGAGTTTTGGCGCGGAACAAGGTTC CONTROL CONTRACTOR TANANCE TO CARCOLOGICA CONTROL CONTROL CANADA CONTROL CANADA CONTROL CANADA CONTROL CONTROL CANADA GATALTCAGAAAAGCCCCCAAAACCAGGAAGATTGTATAAGCCAAATACTTAAATTGTAAACGTTAATATTTTGTTAAAATT GETTGENCTCANGNOSATAGTTNCCGGNTANGGGGCDACGGGTGGGGTGAAGGGGGGTTGGTGCNCACAGGGCCAGGTTG GAGGAAGGACCTACAGGAACTGAGATAACTNCAGGGTGAGCTATTAGAAAAGGGCAGGCTTGGGAAAGGGAAAAGGC TTGGT:ATAAAGCCCGCCTTTTTTTT

| A | nnealing site | | Sequence | | | Sequence after digestion |
|----------|------------------|-------------|----------------------------|-----------|----|------------------------------|
| | 1 | 5. | tgtgctcctctttggcttgcttccaa | 3′ | 5' | tgtgctcctctttggcttgcttccaa 3 |
| | | 3' | acacgaggagaaaccgaacgaaggtt | <u>5'</u> | 3, | tt 5' |
| 1 | 2 | 5" | ctggttcttgtctggcttggcccaa | 3' | 5' | ctggttcttgtctggcttggcccaa3' |
| | | 3' | gaccaagaacagaccgaaccgggtt | 5' | 3' | tt 5' |
| 1 | 3 | 5' | ggtcctcgctctgtgtccgttgaa | 3′ | 5' | ggtcctcgctctgtgtccgttgaa3' |
| <u> </u> | | 3' | ccaggagcgagacacaggcaactt | 5' | 3. | tt5' |
| 1 | 4 | 5. | tttgcgtgtcctgtgtcgtcgaa | 3 ' | 5. | |
| <u></u> | | <u> 3·</u> | aaacgcacaggacacagcagctt | 5, | 3. | tt 5' |

Fig 4

| Annealing site | Sequence | Sequence after digestion |
|----------------|---|--|
| 1 | 5' AAtgtgctcctctttggcttgcttCCGC 3' 3' Ttacacgaggagaaaccgaacgaagg 5' | 5' AA 3' Ttacacgaggagaaaccgaacgaagg 5' |
| 2 | 5' AActggttcttgtctggcttggcCCGC 3' 3' Ttgaccaagaacagaccgaaccggg 5' | 5' AA 3' 3' Ttgaccaagaacagaccgaaccggg 5' |
| 3 | 5' AAggtectegetetgtgteegttGAGCT 3' 3' Ttecaggagegagacacaggcaac 5' | 5' AA 3' Atccaggagcgagacacaggcaac 5' |
| 4 | 5' AAtttgegtgtcctgtgtcgtcGAGCT 3' 3' Ttaaacgcacaggacacagcagc 5' | 5' AA 3' 3' Ttaaacgcacaggacacagcagc 5' |

Fig 5

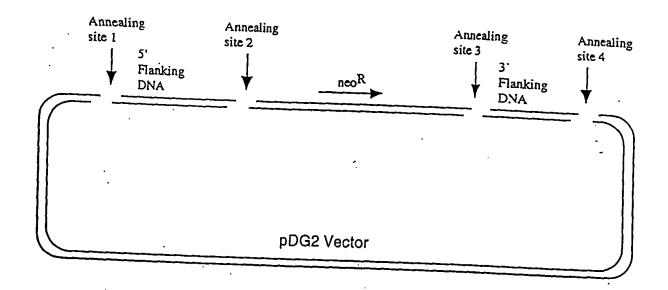


Fig 6

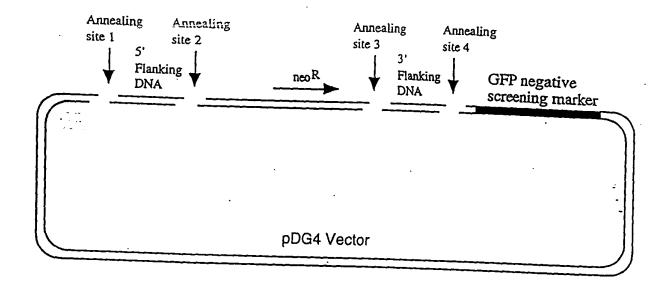


Fig 7

| Oligo# | Sequence (5' to 3') | | | | | | | |
|--------|--|--|--|--|--|--|--|--|
| 174 | ATGACCGCTCAGGAAACCTGTTGCA | | | | | | | |
| 180 | ATAGGCATAGTAGGCCAGCTTGAGG | | | | | | | |
| 454 | tgtgctcctctttggcttgcttccAATTAACCCTCACTAAAGGGAACGAAT | | | | | | | |
| 463 | ctggttcttgtctggcttggcccaaTGCAACAGGTTTCCTGAGCGGTCAT | | | | | | | |
| 464 | ggtcctcgctctgtgtccgttgaaCCTCAAGCTGGCCTACTATGCCTAT | | | | | | | |
| 42 | tttgcgtgtcctgtgtcgtcgaaCGACTAATACGACTCACTATAGGGCG | | | | | | | |
| 151 | GCCAATGGACTCTTAGTTTTGGAAC | | | | | | | |
| 155 | GTTCTGGCAAACAAATTCGGCGCAC | | | | | | | |
| 454 | tgtgctcctctttggcttgcttccAATTAACCCTCACTAAAGGGAACGAAT | | | | | | | |
| 465 | ctggttcttgtctggcttggcccaaGTTCCAAAACTAAGAGTCCATTGGC | | | | | | | |
| 466 | ggtcctcgctctgtgtccgttgaaGTGCGCCGAATTTGTTTGCCAGAAC | | | | | | | |
| 1 | GAACCTTGGTGTGCCAAGTTACTTC | | | | | | | |
| 2 | GAACTTTGGCTGAACCCCTTGTTCT | | | | | | | |
| 41 | . tgtgctcctctttggcttgcgttgaaCGACTAATACGACTCACTATAGGGCG | | | | | | | |
| 38 | ctggttcttgtctggcttggcccaaGAAGTAACTTGGCACACCAAGGTTC | | | | | | | |
| 40 | ggtcctcgctctgtgtccgttgaAGAACAAGGGGTTCAGCCAAAGTTC | | | | | | | |
| 37 | tttgcgtgtcctgtgtcgtcgAATTAACCCTCACTAAAGGGAACGAAT | | | | | | | |
| 540 | ATGCCGGATCTCCTACTGCGCC | | | | | | | |
| 546 | TGTCATAGTAGACAGCGATGGAACG | | | | | | | |
| 445 | GACAAGAACCAGTTGACGTCAAGCTTCCCGGGACGCGTGCTAGCGGCGCGCGC | | | | | | | |
| 667 | ctggttcttgtctggcttggcccaaGGCCCAGTAGTAGGAGATCCGGCAT | | | | | | | |
| 668 | ggtcctcgctctgtgtccgttgaaCGTTCCATCGCTGTCTACTATGACA | | | | | | | |
| 907 | ctggttcttgtctggcttggccaaAAAGCCGACAGCCACGCTCACAAGC | | | | | | | |
| 908 | ggtcctcgctctgtgtccgttgaaGCCCAATGCCACAGAGACAGAATGT | | | | | | | |
| 1157 | ctggttcttgtctggcttggcccaaGTTGGATCCTCTCCAAGGCCCCATCT | | | | | | | |
| 1158 | ggtcctcgctctgtgtccgttgaaCTCCAGTGCCGAGTGTGTGGGGACAG | | | | | | | |

Figure 8